SEP 1'5 2003 &

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: Hinuma, Shuji Habata, Yugo Kawamata, Yuji Hosoya, Masaki Fujii, Ryo Fukusumi, Shoji
- (ii) TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
- (iii) NUMBER OF SEQUENCES: 140
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 - (B) STREET: 130 Water Street

Kitada, Chieko

- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/776,971
 - (B) FILING DATE: 07-FEB-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/JP96/03821
 - (B) FILING DATE: 28-DEC-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 7/343371
 - (B) FILING DATE: 28-DEC-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8/59419
 - (B) FILING DATE: 15-MAR-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8/211805
 - (B) FILING DATE: 12-AUG-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: JP 8/246573
 - (B) FILING DATE: 18-SEP-1996
- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Conlin, David G.
- (B) REGISTRATION NUMBER: 27,026
- (C) REFERENCE/DOCKET NUMBER: 47176

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-523-3400
- (B) TELEFAX: 617-523-6440
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Gly Leu 1 5 10 15

Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile 20 25 30

Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
35 40 45

Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro 50 55 60

Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly 65 70 75 80

Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val 85 90 95

Gln Glu

- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	CCCCCGACAT	CAACCCTGCC	120
TGGTACGCRG	GCCGTGGGAT	CCGGCCCGTG	GGCCGCTTCG	GCCGGCGAAG	AGCTGCCCYG	180
GGGGACGGAC	CCAGGCCTGG	CCCCCGGCGT	GTGCCGGCCT	GCTTCCGCCT	GGAAGGCGGY	240
GCTGAGCCCT	CCCGAGCCCT	CCCGGGGCGG	CTGACGGCCC	AGCTGGTCCA	GGAA	294

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn 1 5 10 15

Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly 25

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro 1 5 10 15
Val Gly Arg

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn

1 5 10 15

Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn 1 5 10 . 15
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly 20 25 30

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn 1 5 10 15

Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly 25 30

Arg

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro 1 5 10 15

Val Gly Arg Phe 20

- (2) INFORMATION FOR SEO ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro 1 5 10 15

Val Gly Arg Phe Gly 20

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro 1 5 10 15

Val Gly Arg Phe Gly Arg

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC GCRGGCCGTG GGATCCGGCC CGTGGGC	60 87
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGC	57
(2) INFORMATION FOR SEQ ID NO:13:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTC	60 93
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 96 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGC	60 96
(2) INFORMATION FOR SEQ ID NO:15:(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 99 base pairs(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGCCGG	60 99
(2) INFORMATION FOR SEQ ID NO:16:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC	60
(2) INFORMATION FOR SEQ ID NO:17:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC GGC	60 63
(2) INFORMATION FOR SEQ ID NO:18:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 66 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGCTTC GGCCGG	60 66

- (2) INFORMATION FOR SEQ ID NO:19:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

- (2) INFORMATION FOR SEQ ID NO:20:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 amino acids

- (B) TYPE: amino acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

1				5					10					15	Ser
			20					25					30	Glu	Ala
		35					40					45	Ala		Thr
	50					55					60				Val
65					70					75					Leu 80
				85					90					95	Asn
			100					105					110		Ala
		115					120					125			Val
	130				Cys	135					140				
145					150					155					Tyr 160
				165	Pro				170					175	
			180		Ala			185					190		
		195			Thr		200					205			
	210				Phe	215					220				
225					Leu 230					235					240
				245	Val				250					255	
			260		Thr			265					270		
		275			Cys		280					285			
	290				Leu	295					300				
Pro 305	His	Ala	Ile	Asp	Pro 310	Tyr	Ala	Phe	Gly	Leu 315	Val	Gln	Leu		Cys 320
His	Trp	Leu	Ala	Met 325	Ser	Ser	Ala	Cys	Tyr 330	Asn	Pro	Phe	Ile	Tyr 335	Ala
Trp	Leu	His	Asp 340	Ser	Phe	Arg	Glu	Glu 345		Arg	Lys	Leu	Leu 350	Val	Ala
Trp	Pro	Arg 355	Lys	Ile	Ala	Pro	His 360		Gln	Asn	Met	Thr 365	Val	Ser	Val
Val	Ile											202			

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn

1 10 15

Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
20 25 30

Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val

Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr 50 55 60

Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr 65 70 75 80

Val Val Leu Val His Pro Leu Arg Arg Ile Ser Leu Arg Leu Ser 85 90 95

Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu 100 105 110

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val 115 120 125

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu 130 135 140

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val 145 150 155 160

Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165 170 175

Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
180 185 190

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	ои о	:23:						
Val 1	Val	Leu	Val	His 5	Pro	Leu	Arg	Arg	Arg 10	Ile	Ser	Leu	Arg	Leu 15	Ser	
Ala	Tyr	Ala	Val 20	Leu	Gly	Ile	Trp	Ala 25		Ser	Ala	Val		Ala	Leu	
Pro	Ala	Ala 35		His	Thr	Tyr	His		Glu	Leu	Lys		30 His	Asp	Val	
Ser	Leu 50		Glu	Glu	Phe	Trp		Ser	Gln	Glu		45 Gln	Arg	Gln	Ile	
Tyr 65		Trp	Gly	Leu	Leu 70	Leu	Gly	Thr	Tyr	Leu 75	60 Leu	Pro	Leu	Leu		
	Leu	Leu	Ser	Tyr 85	. •	Arg	Val	Ser			Leu	Arg	Asn		80 Val	
Val	Pro	Gly	Ser 100		Thr	Gln	Ser		90 Ala	Asp	Trp	Asp	Arg	95 Ala	Arg	
Arg	Arg	Arg 115		Phe	Cys	Leu	Leu 120	105 Val	Val	Val	Val	Val 125	110 Val			
							120	-				125				
		(2)	INF	ORMA	TION	FOR	SEÇ) ID	NO:2	4:						
 (2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 273 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 																
(ii)	MOLE	CULE	TYF	E: c	DNA										
(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	24:						
GCCT	TGGC TCGA CGGT	CT T GC C CA C	GTCC ACGC CGTC	GACG GGCT TATG	T GC G GG T GT	TCAT TGTT CGGT	GTGC CGGC GTTC	ACC GGC ACG	GCCT GGCC'	GCG TGT	TGCC GCCA	GCTC CCTG	AC G GT C	CTGG TTCT	TCGGC CCTAT TCCTG GGTAC	60 120 180 240 273
		(2)	INF	ORMA	TION	FOR	SEQ	ID I	NO:2	5:						
		(A) (B) (C) (D)	LENG TYP: STR.	GTH: E: n ANDE	177 ucle: DNES: Y: l:	ERIS' base ic ac S: do inear	e pa cid ouble	irs								
			CULE													
						CION:										
GGCCT GTGT(TGGG	CAGTO	JA AC	GCTC(CGCA	A CCC	SCGTO	GTG	CCGC	GCTG	CG T	GACC	CAGZ	G CC	ישמממי	CCGG CGAC	60 120 177

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1110 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGGCCTCAT	CGACCACTCG	GGGCCCCAGG	GTTTCTGACT	TATTTTCTGG	GCTGCCGCCG	60
GCGGTCACAA	CTCCCGCCAA	CCAGAGCGCA	GAGGCCTCGG	CGGGCAACGG	GTCGGTGGCT	120
GGCGCGGACG	CTCCAGCCGT	CACGCCCTTC	CAGAGCCTGC	AGCTGGTGCA	TCAGCTGAAG	180
GGGCTGATCG	TGCTGCTCTA	CAGCGTCGTG	GTGGTCGTGG	GGCTGGTGGG	CAACTGCCTG	240
CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGCACAACG	TGACGAACTT	CCTCATCGGC	300
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	360
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	420
CAGCCGGTCA	CCGTCTATGT	GTCGGTGTTC	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	480
GTCGTGCTGG	TGCACCCGCT	GAGGCGGCGC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	540
CTGGCCATCT	GGGCGCTGTC	CGCGGTGCTG	GCGCTGCCCG	CCGCCGTGCA	CACCTATCAC	600
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	660
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	720
ATCCTCCTGT	CTTACGTCCG	GGTGTCAGTG	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCTGC	780
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	840
GTGGTGGTCG	TGGTGGTGTT	CGCCGTCTGC	TGGCTGCCGC	TGCACGTCTT	CAACCTGCTG	900
CGGGACCTCG	ACCCCCACGC	CATCGACCCT	TACGCCTTTG	GGCTGGTGCA	GCTGCTCTGC	960
CACTGGCTCG	CCATGAGTTC	GGCCTGCTAC	AACCCCTTCA	TCTACGCCTG	GCTGCACGAC	1020
	AGGAGCTGCG	CAAACTGTTG	GTCGCTTGGC	CCCGCAAGAT	AGCCCCCCAT	1080
GGCCAGAATA	TGACCGTCAG	CGTGGTCATC				1110

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGTGCTGG	TGATCGCGCG	GGTGCGCCGG	CTGTACAACG	TGACGAATTT	CCTCATCGGC	60
AACCTGGCCT	TGTCCGACGT	GCTCATGTGC	ACCGCCTGCG	TGCCGCTCAC	GCTGGCCTAT	120
GCCTTCGAGC	CACGCGGCTG	GGTGTTCGGC	GGCGGCCTGT	GCCACCTGGT	CTTCTTCCTG	180
CAGGCGGTCA	CCGTCTATGT	GTCGGTGTTC	ACGCTCACCA	CCATCGCAGT	GGACCGCTAC	240
GTCGTGCTGG	TGCACCCGCT	GAGGCGCCC	ATCTCGCTGC	GCCTCAGCGC	CTACGCTGTG	300
CTGGCCATCT	GGGTGCTGTC	CGCGGTGCTG	GCGCTGCCCG	CCGCCGTGCA	CACCTATCAC	360
GTGGAGCTCA	AGCCGCACGA	CGTGCGCCTC	TGCGAGGAGT	TCTGGGGCTC	CCAGGAGCGC	420
CAGCGCCAGC	TCTACGCCTG	GGGGCTGCTG	CTGGTCACCT	ACCTGCTCCC	TCTGCTGGTC	480
ATCCTCCTGT	CTTACGCCCG	GGTGTCAGTG	AAGCTCCGCA	ACCGCGTGGT	GCCGGGCCGC	540
GTGACCCAGA	GCCAGGCCGA	CTGGGACCGC	GCTCGGCGCC	GGCGCACCTT	CTGCTTGCTG	600
GTGGTGGTCG	TGGTGGTG					618

(2) INFORMATION FOR SEQ ID NO:28:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 378 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT GTGGAGCTCA AGCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC ATCCTCCTGT CTTACGTACG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG GTGGTGGTGGT TGGTAGTG	60 120 180 240 300 360 378
(2) INFORMATION FOR SEQ ID NO:29:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
CGTGGSCMTS STGGGCAACN YCCTG	25
(2) INFORMATION FOR SEQ ID NO:30:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GTNGWRRGGC ANCCAGCAGA KGGCAAA	27
(2) INFORMATION FOR SEQ ID NO:31:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs	

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
CTGTGY	GYSA TYGCNNTKGA YMGSTAC	27
	(2) INFORMATION FOR SEQ ID NO:32:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:32:	
AKGWAGW	NAGG GCAGCCAGCA GANSRYGAA	29
	(2) INFORMATION FOR SEQ ID NO:33:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:33:	
CTGACTT	ATT TTCTGGGCTG CCGC	24
	(2) INFORMATION FOR SEQ ID NO:34:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:34:	

(B) TYPE: nucleic acid

20

- (2) INFORMATION FOR SEQ ID NO:35:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: modified base
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /mod_base= i.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCNCAYCARC AYTGYATGGA

- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /mod_base= i
- (ix) FEATURE:
 - (A) NAME/KEY: modified base
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /mod_base= i
- (ix) FEATURE:
 - (A) NAME/KEY: modified base
 - (B) LOCATION: 18
 - (D) OTHER INFORMATION: /mod_base= i
- (ix) FEATURE:
 - (A) NAME/KEY: modified_base
 - (B) LOCATION: 24
 - (D) OTHER INFORMATION: /mod_base= i
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

- (2) INFORMATION FOR SEQ ID NO:37: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA" (ix) FEATURE: (A) NAME/KEY: modified base (B) LOCATION: 15 (D) OTHER INFORMATION: /mod_base= i (ix) FEATURE: (A) NAME/KEY: modified_base (B) LOCATION: 21 (D) OTHER INFORMATION: /mod_base= i (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: ACGGGCCKDA TGCCNCKGCC NGCRTA 26 (2) INFORMATION FOR SEQ ID NO:38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA" (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38: CCGGCGTACC AGGCAGGGTT 20 (2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

(A) DESCRIPTION: /desc = "synthetic DNA"

(ii) MOLECULE TYPE: other nucleic acid

(D) TOPOLOGY: linear

	(2) INFORMATION FOR SEQ ID NO:40:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CTGCCAG	GCAG AGCCCACCAG CACTCCA	. 27
	(2) INFORMATION FOR SEQ ID NO:41:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:41:	
GTGGGGG	SCCT GGCTCCTCTG CCTGCTG	27
	(2) INFORMATION FOR SEQ ID NO:42:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:	
GTGTCGAG	CGA ATGAAGGCGG TGGGGGCCTG GC	32
	(2) INFORMATION FOR SEQ ID NO:43:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid	

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGGCTCCCGC TGTTATTCCT GGAC

24

- (2) INFORMATION FOR SEQ ID NO:44:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear .
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Gly Leu 10 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile

25 Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg

40 Pro Val Gly Arg Phe Gly Arg Arg Ala Ala Leu Gly Asp Gly Pro

Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly

Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val 85 90

Gln Glu

- (2) INFORMATION FOR SEQ ID NO:45:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Ser Leu Val 10 Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg

Thr	Pro	Asp 35	Ile	Asn	Pro	Ala	Trp	Tyr	Thr	Gly	Arg	Gly 45	Ile	Arg	Pro	
Val	Gly 50	Arg	Phe	Gly	Arg	Arg 55	Arg	Ala	Thr	Pro	Arg 60	Asp	Val	Thr	Gly	
65			Leu	Ser	Cys 70	Leu	Pro	Leu	Asp	Gly 75	Arg	Thr	Lys	Phe	Ser 80	
GIN	Arg	GIY														
		(2)	INI	FORM	OIT	1 FOI	R SE(O ID	NO:4	16:						
	(i)	(A) (B) (C)	LEN TYI STI	E CHA NGTH: PE: 1 RANDE POLOC	: 249 nucle EDNES	baseic a	se pa acid doub]	airs								
	(ii) MOLECULE TYPE: cDNA															
	(xi)	SEQU	JENCI	E DES	CRIE	OIT	1: SE	EQ II	ON C	46:						
TCCA TACA GATO	AGGGG	BAG C BCC G ETG G	CCA(CCAGO BATCA	CA CI	CCAT	rggac rgggc	ACA C CGC	AAGAZ CTTCC	ACCC GCA	CTGA GGA	ATATO BAAGO	CAA :	TCCT(GGGGCT GCCTGG CCGAGG FTCTCT	60 120 180 240 249
		(2)	INE	FORMA	MOITA	I FOF	SEÇ) ID	NO:4	17:						
	(i)	(A) (B) (C)	LEN TYI STI	E CHA IGTH: PE: & RANDE POLOG	31 minc DNES	amin aci S: s	no ac .d singl	ids								
((ii)	MOLE	CULE	TYF	E: p	rote	in									
((v) F	'RAGM	ENT	TYPE	: in	tern	al									
((xi)	SEQU	ENCE	DES	CRIF	TION	: SE	Q II	NO:	47:						
Ser 1	Arg	Ala	His	Gln 5	His	Ser	Met	Glu	Thr 10	Arg	Thr	Pro	Asp	Ile 15	Asn	

25

(2) INFORMATION FOR SEQ ID NO:48:

Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn

1 5 10 15

Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

- (2) INFORMATION FOR SEQ ID NO:49:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn 1 5 10 15

Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly 25 30

Arg

- (2) INFORMATION FOR SEQ ID NO:50:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro

1 5 10 15

Val Gly Arg Phe
20

- (2) INFORMATION FOR SEQ ID NO:51:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids

(B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(v) FRAGMENT TYPE: internal	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro 1 5 10 15 Val Gly Arg Phe Gly 20	
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(v) FRAGMENT TYPE: internal	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro 1 5 10 15 Val Gly Arg Phe Gly Arg 20	
(2) INFORMATION FOR SEQ ID NO:53:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTC	60 93
(2) INFORMATION FOR SEQ ID NO:54:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 96 base pairs(B) TYPE: nucleic acid	

	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:54:	
	CCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC GCG GGATCAGGCC TGTGGGCCGC TTCGGC	60 96
	(2) INFORMATION FOR SEQ ID NO:55:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:55:	
		60 99
	(2) INFORMATION FOR SEQ ID NO:56:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 60 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:56:	
ACCCCTG	ATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC	60
	(2) INFORMATION FOR SEQ ID NO:57:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 63 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:57:	
ACCCCTG# GGC		60 63

(C) STRANDEDNESS: double

	(2)	INFORMATION FOR SEQ ID NO:58:
(i)	(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 66 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
(2.2)		

- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC GGCAGG

60

66

.(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

 Met
 Lys
 Val
 Leu
 Arg
 Ala
 Trp
 Leu
 Cys
 Leu
 Leu
 Met
 Leu
 Gly
 Leu

 Ala
 Leu
 Arg
 Gly
 Ala
 Ala
 Ser
 Arg
 Thr
 His
 Ser
 Met
 Glu
 Ile

 Arg
 Thr
 Pro
 Arg
 His
 Ser
 Met
 Glu
 Ile

 Arg
 Thr
 Pro
 Arg
 Trp
 Tyr
 Ala
 Ser
 Arg
 Gly
 Ile
 Arg

 Pro
 Val
 Gly
 Arg
 Pro
 Arg
 Arg

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGAAGGTGC	TGAGGGCCTG	GCTCCTGTGC	CTGCTGATGC	TGGGCCTGGC	CCTGCGGGGA	60
GCTGCAAGTC	GTACCCATCG	GCACTCCATG	GAGATCCGCA	CCCCTGACAT	CAATCCTGCC	120
TGGTACGCCA	GTCGCGGGAT	CAGGCCTGTG	GGCCGCTTCG	GTCGGAGGAG	GGCAACCCTG	180
GGGGACGTCC	CCAAGCCTGG	CCTGCGACCC	CGGCTGACCT	GCTTCCCCCT	GGAAGGCGGT	240
GCTATGTCGT	CCCAGGATGG	C				261

- (2) INFORMATION FOR SEQ ID NO:61:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn

1 5 10 15

Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

- (2) INFORMATION FOR SEQ ID NO:62:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn 1 5 10 15

Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly 20 25 30

- (2) INFORMATION FOR SEQ ID NO:63:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn 1 5 10 15

Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly 20 25 30

Arg

- (2) INFORMATION FOR SEQ ID NO:64:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro 1 5 10 15

Val Gly Arg Phe 20

- (2) INFORMATION FOR SEO ID NO:65:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro 1 5 10 15

Val Gly Arg Phe Gly 20

- (2) INFORMATION FOR SEQ ID NO:66:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(ii)	MOLECULE TYPE: protein	
(v)	FRAGMENT TYPE: internal	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:66:	
1	Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro 5 10 15 Arg Phe Gly Arg 20	
(i)	(2) INFORMATION FOR SEQ ID NO:67: SEQUENCE CHARACTERISTICS: (A) LENGTH: 93 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:67:	
	CCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC GCG GGATCAGGCC TGTGGGCCGC TTC	60 93
	(2) INFORMATION FOR SEQ ID NO:68:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 96 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:68:	
AGTCGTAC GCCAGTCC	CCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC GCG GGATCAGGCC TGTGGGCCGC TTCGGT	60 96
	(2) INFORMATION FOR SEQ ID NO:69:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:69:	

(D) TOPOLOGY: linear

GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTCGGTCGG	CATCAATCC TGCCTGGTAC 60 99
(2) INFORMATION FOR SEQ ID NO:70:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 60 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA T	CAGGCCTGT GGGCCGCTTC 60
(2) INFORMATION FOR SEQ ID NO:71:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 63 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCGGT	CAGGCCTGT GGGCCGCTTC 60 63
(2) INFORMATION FOR SEQ ID NO:72:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 66 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TC GGTCGG	CAGGCCTGT GGGCCGCTTC 60
(2) INFORMATION FOR SEQ ID NO:73:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 amino acids	

(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /product= "Ala or Thr"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 11
 - (D) OTHER INFORMATION: /product= "Gly or Ser"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 21..22
 - (D) OTHER INFORMATION: /product= "may be a Gly-Arg or Gly"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Xaa Arg Gly Ile Arg Pro 1 5 10 15
Val Gly Arg Phe Xaa Xaa 20

- (2) INFORMATION FOR SEQ ID NO:74:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /product= "Ala or Thr"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /product= "Gln or Arg"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /product= "Ile or Thr"

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:74:	
Ser Arg	y Xaa His Xaa His Ser Met Glu Xaa Arg 5 10	
	(2) INFORMATION FOR SEQ ID NO:75:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:75:	
CARCAYT	CCA TGGAGACAAG AACCCC	26
	(2) INFORMATION FOR SEQ ID NO:76:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:76:	
TACCAGG	CAG GATTGATACA GGGG	24
	(2) INFORMATION FOR SEQ ID NO:77:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:77:	
GGCATCAT	TCC AGGAAGACGG AGCAT	25
	(2) INFORMATION FOR SEQ ID NO:78:	
(i)	SEQUENCE CHARACTERISTICS:	

	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:78:	
AGCAGAG	GGAG AGGGAGGGTA GAGGA	25
	(2) INFORMATION FOR SEQ ID NO:79:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:79:	
ACGTGGC	TTC TGTGCTTGCT GC	22
	(2) INFORMATION FOR SEQ ID NO:80:	
(1)	SEQUENCE CHARACTERISTICS:	
(1)	(A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:80:	
GCCTGAT(CCC GCGGCCCGTG TACCA	25
	(2) INFORMATION FOR SEQ ID NO:81:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:81:	

(A) LENGTH: 25 base pairs

	(2) INFORMATION FOR SEQ ID NO:82:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GGCGGG	GCT GCAAGTCGTA CCCATCG	2′
	(2) INFORMATION FOR SEQ ID NO:83:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:83:	
CGGCACT	CCA TGGAGATCCG CACCCCT	27
	(2) INFORMATION FOR SEQ ID NO:84:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:84:	
CAGGCAG	GAT TGATGTCAGG GGTGCGG	27
	(2) INFORMATION FOR SEQ ID NO:85:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid	

	STRANDEDNESS: single TOPOLOGY: linear	
	CCULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"	
(xi) SEQU	JENCE DESCRIPTION: SEQ ID NO:85:	
CATGGAGTGC C	GATGGGTAC GACTTGC	27
(2)	INFORMATION FOR SEQ ID NO:86:	
	ENCE CHARACTERISTICS:	
	LENGTH: 27 base pairs TYPE: nucleic acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	CULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"	
(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:86:	
GGCCTCCTCG G	AGGAGCCAA GGGATGA	27
(2)	INFORMATION FOR SEQ ID NO:87:	
(i) SEOU	ENCE CHARACTERISTICS:	
	LENGTH: 27 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: single	
(D)	TOPOLOGY: linear	
	CULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"	
(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO:87:	
CCCA A A CCA C	CCGAAGGAG AGGAGAG	
GGGAAAGGAG C	CCGAAGGAG AGGAGAG	27
(2)	INFORMATION FOR SEQ ID NO:88:	
(i) SEQU	ENCE CHARACTERISTICS:	
	LENGTH: 25 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: single TOPOLOGY: linear	
(ii) MOLE	CULE TYPE: other nucleic acid	
	DESCRIPTION: /desc = "synthetic DNA"	
(xi) SEQUI	ENCE DESCRIPTION: SEQ ID NO:88:	
CCTGCTGGCC A	TTCTCCTGT CTTAC	25

	(2)	INFORMATION FOR SEQ ID NO:89:	
(i)	(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(ii)		CULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQU	ENCE DESCRIPTION: SEQ ID NO:89:	
GGGTCCA	GGT C	CCGCAGAAG GTTGA	25
	(2)	INFORMATION FOR SEQ ID NO:90:	
(i)	(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(ii)		CULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQU	ENCE DESCRIPTION: SEQ ID NO:90:	
GAAGACG	GAG C	ATGGCCCTG AAGAC	25
	(2)	INFORMATION FOR SEQ ID NO:91:	
(i)	SEQU (A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear	
(ii)		CULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"	
(xi)	SEQU	ENCE DESCRIPTION: SEQ ID NO:91:	
GGCAGCT	GAG T	TGGCCAAGT CCAGT	25
	(2)	INFORMATION FOR SEQ ID NO:92:	
(i)	(A) (B) (C)	ENCE CHARACTERISTICS: LENGTH: 15 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear	

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Cys

1 10 15

- (2) INFORMATION FOR SEQ ID NO:93:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:94:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Cys Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:95:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"

24

- (2) INFORMATION FOR SEQ ID NO:96:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTCAGAGCTA GCAGAGTGTC ATCAG

25

- (2) INFORMATION FOR SEQ ID NO:97:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15

Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

- (2) INFORMATION FOR SEQ ID NO:98:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro

1 5 10 15

Val Gly Arg Phe

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 669 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...669
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

			_						×		<i>_</i>						
GTG Val 1	GGC Gly	ATG Met	GTG Val	GGC Gly 5	AAC Asn	ATC Ile	CTG Leu	CTG Leu	GTG Val 10	CTG Leu	GTG Val	ATC Ile	GCG Ala	CGG Arg	GTG Val	48	
CGC Arg	CGG Arg	CTG Leu	TAC Tyr 20	AAC Asn	GTG Val	ACG Thr	AAT Asn	TTC Phe 25	CTC Leu	ATC Ile	GGC Gly	AAC Asn	CTG Leu 30	GCC Ala	TTG Leu	96	
TCC Ser	GAC Asp	GTG Val 35	CTC Leu	ATG Met	TGC Cys	ACC Thr	GCC Ala 40	TGC Cys	GTG Val	CCG Pro	CTC Leu	ACG Thr 45	CTG Leu	GCC Ala	TAT Tyr	144	
GCC Ala	TTC Phe 50	GAG Glu	CCA Pro	CGC Arg	GGC Gly	TGG Trp 55	GTG Val	TTC Phe	GGC Gly	GGC Gly	GGC Gly 60	CTG Leu	TGC Cys	CAC His	CTG Leu	192	
GTC Val 65	TTC Phe	TTC Phe	CTG Leu	CAG Gln	GCG Ala 70	GTC Val	ACC Thr	GTC Val	TAT Tyr	GTG Val 75	TCG Ser	GTG Val	TTC Phe	ACG Thr	CTC Leu 80	240	
ACC Thr	ACC Thr	ATC Ile	GCA Ala	GTG Val 85	GAC Asp	CGC Arg	TAC Tyr	GTC Val	GTG Val 90	CTG Leu	GTG Val	CAC His	CCG Pro	CTG Leu 95	AGG Arg	288	
CGG Arg	CGC Arg	ATC Ile	TCG Ser 100	CTG Leu	CGC Arg	CTC Leu	AGC Ser	GCC Ala 105	TAC Tyr	GCT Ala	GTG Val	CTG Leu	GCC Ala 110	ATC Ile	TGG Trp	336	
GTG Val	CTG Leu	TCC Ser 115	GCG Ala	GTG Val	CTG Leu	GCG Ala	CTG Leu 120	CCC Pro	GCC Ala	GCC Ala	GTG Val	CAC His 125	ACC Thr	TAT Tyr	CAC His	384	
GTG Val	GAG Glu 130	CTC Leu	AAG Lys	CCG Pro	CAC His	GAC Asp 135	GTG Val	CGC Arg	CTC Leu	TGC Cys	GAG Glu 140	GAG Glu	TTC Phe	TGG Trp	GGC Gly	432	
TCC Ser 145	CAG Gln	GAG Glu	CGC Arg	CAG Gln	CGC Arg 150	CAG Gln	CTC Leu	TAC Tyr	GCC Ala	TGG Trp 155	GGG Gly	CTG Leu	CTG Leu	CTG Leu	GTC Val 160	480	
ACC Thr	TAC Tyr	CTG Leu	CTC Leu	CCT Pro 165	CTG Leu	CTG Leu	GTC Val	ATC Ile	CTC Leu 170	CTG Leu	TCT Ser	TAC Tyr	GCC Ala	CGG Arg 175	GTG Val	528	

TCA Ser	GTG Val	AAG Lys	CTC Leu 180	CGC Arg	AAC Asn	CGC Arg	GTG Val	GTG Val 185	CCG Pro	GGC Gly	CGC Arg	GTG Val	ACC Thr 190	CAG Gln	AGC Ser	576
CAG Gln	GCC Ala	GAC Asp 195	TGG Trp	GAC Asp	CGC Arg	GCT Ala	CGG Arg 200	CGC Arg	CGG Arg	CGC Arg	ACC Thr	TTC Phe 205	TGC Cys	TTG Leu	CTG Leu	624
GTG Val	GTG Val 210	GTC Val	GTG Val	GTG Val	GTG Val	TTC Phe 215	ACC Thr	CTC Leu	TGC Cys	TGG Trp	CTG Leu 220	CCC Pro	TTC Phe	TTC Phe		669

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Va I	Clyr	Mot	17.01	a1	3	~7.	.	_		_	_	_			
T	Gly			5					10					15	
Arg	Arg	Leu	Tyr 20	Asn	Val	Thr	Asn	Phe 25	Leu	Ile	Gly	Asn	Leu 30	Ala	Leu
Ser	Asp	Val 35	Leu	Met	Cys	Thr	Ala 40	Cys	Val	Pro	Leu	Thr 45	Leu	Ala	Tyr
Ala	Phe 50	Glu	Pro	Arg	Gly	Trp 55	Val	Phe	Gly	Gly	Gly 60		Cys	His	Leu
Val 65	Phe	Phe	Leu	Gln	Ala 70	Val	Thr	Val	Tyr	Val 75		Val	Phe	Thr	Leu 80
Thr	Thr	Ile	Ala	Val 85	Asp	Arg	Tyr	Val	Val 90		Val	His	Pro	Leu 95	Arg
Arg	Arg	Ile	Ser 100	Leu	Arg	Leu	Ser	Ala 105	Tyr	Ala	Val	Leu	Ala 110	Ile	Trp
Val	Leu	Ser 115	Ala	Val	Leu	Ala	Leu 120	Pro	Ala	Ala	Val	His 125	Thr	Tyr	His
Val	Glu 130	Leu	Lys	Pro	His	Asp		Arg	Leu	Cys	Glu 140	Glu	Phe	Trp	Gly
Ser 145	Gln	Glu	Arg	Gln	Arg 150	Gln	Leu	Tyr	Ala	Trp 155		Leu	Leu	Leu	Val 160
Thr	Tyr	Leu	Leu	Pro 165	Leu	Leu	Val	Ile	Leu 170		Ser	Tyr	Ala	Arg 175	Val
Ser	Val	Lys	Leu 180	Arg	Asn	Arg	Val	Val 185	Pro	Gly	Arg	Val	Thr 190		Ser
Gln	Ala	Asp 195	Trp	Asp	Arg	Ala	Arg 200		Arg	Arg	Thr	Phe 205		Leu	Leu
Val	Val 210	Val	Val	Val	Val	Phe 215		Leu	Cys	Trp	Leu 220	Pro	Phe	Phe	

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val 10 Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu 25 Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr 40 Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Leu Cys His Leu 55. Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu 75 Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg 90 Arg Arg Ile Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val 100 105 Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val 120 Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg 135 Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala 150 Ile Cys Trp Leu Pro Tyr Tyr 165

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

 Val
 Gly
 Met
 Val
 Gly
 Asn
 Ile
 Leu
 Leu
 Val
 Leu
 Val
 Ile
 Ala
 Arg
 Val

 1

_			100					105					110			
		115					120					125		_	His	
	130					135					140)		_	Gly	
Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala			Leu	Let	Leu	val	
145 Thr		Leu	Leu	Pro 165			Val	Ile	Leu 170			Tyr	Ala		160 Val	
Ser	Val	Lys	Leu 180			Arg	Val	Val	Pro		Arg	Val	Thr		Ser	
Gln	Ala	Asp 195	Trp	Asp	Arg	Ala	Arg 200	Arg		Arg	Thr	Phe	Cys		Leu	
Val	Val 210		Val	Val	Val	Phe 215	Thr	Leu	Cys	Trp	Leu 220	Pro	Phe	Phe	:	
Carry	(:	i) Si (A) (B) (C) (D) ix) 1 (A) (B) (D)	EQUED LENG TYPE STRATOPO	NCE (GTH: E: IN ANDER DLOG!) JRE: ME/KI CATIC HER I	CHAR 133 ucle DNES Y: 1 EY: 0 DN: DESG	N FOR ACTER 1 bas ic ac S: s: inear 1 la	RIST: se pacid ingle r ng Se 122 ION:	ICS: airs e equer 27	nce Q ID	NO:						
CTG	CCCC	AAG (CAGAT	rgaac cgcg <i>i</i>	SA TO	CATCC 3CTT1	CACGA	A GGA	ATGG(CTAC AAAC	TCC	GAGG(ACTC(CCA (AGCA(GGTG(GAAATT GCC ATG Met 1	60 120
GCC Ala	TCA Ser	TCG Ser	ACC Thr 5	ACT Thr	CGG Arg	GGC Gly	CCC Pro	AGG Arg 10	GTT Val	TCT Ser	GAC Asp	TTA Leu	TTT Phe 15	TCT Ser	GGG Gly	168
CTG Leu	CCG Pro	CCG Pro 20	GCG Ala	GTC Val	ACA Thr	ACT Thr	CCC Pro 25	GCC Ala	AAC Asn	CAG Gln	AGC Ser	GCA Ala 30	GAG Glu	GCC Ala	TCG Ser	216
GCG Ala	GGC Gly 35	AAC Asn	GGG Gly	TCG Ser	GTG Val	GCT Ala 40	GGC Gly	GCG Ala	GAC Asp	GCT Ala	CCA Pro 45	GCC Ala	GTC Val	ACG Thr	CCC Pro	264
Phe 50	Gln	Ser	Leu	Gln	Leu 55	GTG Val	His	Gln	Leu	Lys 60	Gly	Leu	Ile	Val	Leu 65	312
CTC Leu	TAC Tyr	AGC Ser	Val	GTG Val 70	GTG Val	GTC Val	GTG Val	GGG Gly	CTG Leu 75	GTG Val	GGC Gly	AAC Asn	TGC Cys	CTG Leu 80	CTG Leu	360

						GTG Val										408	
						TTG Leu							Thr			456	
						TAT Tyr 120										504	
						CTG Leu										552	
						CTC Leu										600	
						AGG Arg										648	
						TGG Trp										696	
						CAC His 200										744	
						GGC Gly										792	
						GTC Val										840	
CTC Leu	CTG Leu	TCT Ser	TAC Tyr 245	GTC Val	CGG Arg	GTG Val	TCA Ser	GTG Val 250	AAG Lys	CTC Leu	CGC Arg	AAC Asn	CGC Arg 255	GTG Val	GTG Val	888	
CCG Pro	GGC Gly	TGC Cys 260	GTG Val	ACC Thr	CAG Gln	AGC Ser	CAG Gln 265	Ala	GAC Asp	TGG Trp	GAC Asp	CGC Arg 270	GCT Ala	CGG Arg	CGC Arg	936	
						CTG Leu 280										984	
TGC Cys 290	TGG Trp	CTG Leu	CCG Pro	CTG Leu	CAC His 295	GTC Val	TTC Phe	AAC Asn	CTG Leu	CTG Leu 300	CGG Arg	GAC Asp	CTC Leu	Asp	CCC Pro 305	1032	

His	Ala	Ile	Asp	Pro 310	TAC Tyr	GCC Ala	TTT	GGG Gly	CTG Leu 315	GTG Val	CAG Gln	CTG Leu	CTC Leu	TGC Cys 320	CAC His	1080
													TAC Tyr 335			1128
													GTC Val			1176
CCC Pro	CGC Arg 355	AAG Lys	ATA Ile	GCC Ala	CCC Pro	CAT His 360	GGC Gly	CAG Gln	AAT Asn	ATG Met	ACC Thr 365	GTC Val	AGC Ser	GTG Val	GTC Val	1224
ATC Ile: 370		GCCA	CT I	AGCC	CAGGC	C TI	GGTC	CAAGG	AGC	TCCA	CTT	CAAC	TGGC	CT C	CTAGG	1283
GCAC	CACT	CG A	GGTC	CAATO	T GG	TGCT	TATI	CTC	AGCA	CCA	GAGC	TAGO	:			1331

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met 1	Ala	Ser	Ser	Thr 5	Thr	Arg	Gly	Pro	Arg 10	Val	Ser	Asp	Leu	Phe 15	Ser
Gly	Leu	Pro	Pro 20	Ala	Val	Thr	Thr		Ala	Asn	Gln	Ser	Ala 30	Glu	Ala
		35					40					45		Val	
	50					55					60	_		Ile	
Leu 65	Leu	Tyr	Ser	Val	Val 70	Val	Val	Val	Gly	Leu 75	Val	Gly	Asn	Сув	Leu 80
				85					90					Thr 95	
Phe	Leu	Ile	Gly 100	Asn	Leu	Ala	Leu	Ser 105	Asp	Val	Leu	Met	Cys 110	Thr	Ala
Cys	Val	Pro 115	Leu	Thr	Leu	Ala	Tyr 120	Ala	Phe	Glu	Pro	Arg 125	Gly	Trp	Val
Phe	Gly 130	Gly	Gly	Leu	Cys	His 135	Leu	Val	Phe	Phe	Leu 140	Gln	Pro	Val	Thr
145					150					155			_	Arg	160
Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg	Arg	Ile	Ser	Leu	Arg	Leu	Ser

				165					170					175	
			180					185					190	Ala	
		195					200					205		Asp	
	210					215					220			Gln	
225					230					235				Leu	240
				245					250					Arg 255	
			260					265					270	Ala	
		275					280					285		Phe	
	290					295					300			Leu	
305					310					315				Leu	320
				325					330					Tyr 335	
			340					345					350	Val	
		Arg 355	Lys	Ile	Ala	Pro	His 360	Gly	Gln	Asn	Met	Thr 365	Val	Ser	Val
Val	Ile 370														

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...432
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CTG Leu 1	TGT Cys	GTC Val	ATC Ile	GCG Ala 5	GTG Val	GAT Asp	AGG Arg	TAC Tyr	GTG Val 10	GTT Val	CTG Leu	GTG Val	CAC His	CCG Pro 15	CTA Leu		48
CGT Arg	CGG Arg	CGC Arg	ATT Ile 20	TCA Ser	CTG Leu	AGG Arg	CTC Leu	AGC Ser 25	GCC Ala	TAC Tyr	GCG Ala	GTG Val	CTG Leu 30	GGC Gly	ATC Ile		96
TGG Trp	GCT Ala	CTA Leu 35	TCT Ser	GCA Ala	GTG Val	CTG Leu	GCG Ala 40	CTG Leu	CCG Pro	GCC Ala	GCG Ala	GTG Val 45	CAC His	ACC Thr	TAC Tyr	1	.44

CAT His	GTG Val 50	GAG Glu	CTC Leu	AAG Lys	CCC Pro	CAC His 55	GAC Asp	GTG Val	AGC Ser	CTC Leu	TGC Cys 60	GAG Glu	GAG Glu	TTC Phe	TGG Trp		192
GGC Gly 65	TCG Ser	CAG Gln	GAG Glu	CGC Arg	CAA Gln 70	CGC Arg	CAG Gln	ATC Ile	TAC Tyr	GCC Ala 75	TGG Trp	GGG Gly	CTG Leu	CTT Leu	CTG Leu 80		240
GGC Gly	ACC Thr	TAT Tyr	TTG Leu	CTC Leu 85	CCC Pro	CTG Leu	CTG Leu	GCC Ala	ATC Ile 90	CTC Leu	CTG Leu	TCT Ser	TAC Tyr	GTA Val 95	CGG Arg		288
GTG Val	TCA Ser	GTG Val	AAG Lys 100	CTG Leu	AGG Arg	AAC Asn	CGC Arg	GTG Val 105	GTG Val	CCT Pro	GGC Gly	AGC Ser	GTG Val 110	ACC Thr	CAG Gln		336
AGT Ser	CAA Gln	GCT Ala 115	GAC Asp	TGG Trp	GAC Asp	CGA Arg	GCG Ala 120	CGT Arg	CGC Arg	CGC Arg	CGC Arg	ACT Thr 125	TTC Phe	TGT Cys	CTG Leu		384
CTG Leu	GTG Val 130	GTG Val	GTG Val	GTG Val	GTA Val	GTG Val 135	TTC Phe	ACG Thr	CTC Leu	TGC Cys	TGG Trp 140	CTG Leu	CCC Pro	TTC Phe	TAC Tyr	С	433
Т																	434

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

1				5					Val 10					15	
Arg	Arg	Arg	Ile 20	Ser	Leu	Arg	Leu	Ser 25	Ala	Tyr	Ala	Val	Leu 30	Gly	Ile
		35					40		Pro			4.5			-
His	Val 50	Glu	Leu	Lys	Pro	His 55	Asp	Val	Ser	Leu	Cys 60	Glu	Glu	Phe	Trp
Gly 65	Ser	Gln	Glu	Arg	Gln 70	Arg	Gln	Ile	Tyr	Ala 75	Trp	Gly	Leu	Leu	Leu 80
Gly	Thr	Tyr	Leu	Leu 85	Pro	Leu	Leu	Ala	Ile 90	Leu	Leu	Ser	Tyr	Val 95	Arg
Val	Ser	Val	Lys 100	Leu	Arg	Asn	Arg	Val 105	Val	Pro	Gly	Ser	Val 110		Gln
Ser	Gln	Ala 115	Asp	Trp	Asp	Arg	Ala 120	Arg	Arg	Arg	Arg	Thr 125	Phe	Cys	Leu
Leu	Val	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp		Pro	Phe	Tvr

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val 10 Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu 75 Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg 90 Arg Arg Ile Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val 105 Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val 120 Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg 135 140 Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala 150 155 Ile Cys Trp Leu Pro Tyr Tyr 165

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

 Val
 Gly
 Met
 Val
 Gly
 Asn
 Ile
 Leu
 Leu
 Val
 Leu
 Val
 Ile
 Ala
 Arg
 Val

 Arg
 Arg
 Leu
 Tyr
 Asn
 Val
 Thr
 Asn
 Phe
 Leu
 Ile
 Gly
 Asn
 Leu
 Ala
 Leu

 Ser
 Asp
 Val
 Leu
 Met
 Cys
 Thr
 Ala
 Cys
 Val
 Pro
 Leu
 Thr
 Leu
 Ala
 Tyr

 Ala
 Phe
 Glu
 Pro
 Arg
 Gly
 Trp
 Val
 Phe
 Gly
 Gly
 Leu
 Cys
 His
 Leu

 Val
 Phe
 Phe
 Leu
 Gl
 Ala
 Val
 Thr
 Val
 Tyr
 Val
 Ser
 Val
 Phe
 Thr
 Leu

 65
 70
 75
 80
 80
 Ala
 Ala</td

Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg 90 Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Ala Ile Trp 105 Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His 120 Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly 135 Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Val 155 Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr Ala Arg Val 165 170 Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser 180 185 Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu Leu 200 Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Phe 210 215

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu 5 10 Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr 40 His Val Glu Leu Lys Pro His Asp Val Ser Leu Cys Glu Glu Phe Trp 55 Gly Ser Gln Glu Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Leu 70 Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg 90 Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln 105 Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu 120 125 Leu Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr 130 135 140

(2) INFORMATION FOR SEQ ID NO:110

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(1X) F	EATURE:		
	NAME/KEY: LOCATION:	_	Sequence
	OTHER INFO		J:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC
Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala
1 5 10 15

TGG TAC GCG GGC CGT GGG ATC CGG CCC G
Trp Tyr Ala Gly Arg Gly Ile Arg Pro
20 25

76

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala

1 5 10 15

Trp Tyr Ala Gly Arg Gly Ile Arg Pro
20 25

- (2) INFORMATION FOR SEQ ID NO:112:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 6...125
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CTG GCC CTG CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG Leu Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu 20 25 30	98
ATC CGC ACC CCC GAC ATC AAC CCT GCC T Ile Arg Thr Pro Asp Ile Asn Pro Ala 35 40	126
(2) INFORMATION FOR SEQ ID NO:113:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein (v) FRAGMENT TYPE: internal	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Gly Leu	
1 5 10 15 Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile	
20 25 30 Arg Thr Pro Asp Ile Asn Pro Ala 35 40	
(2) INFORMATION FOR SEQ ID NO:114:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 380 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ix) FEATURE:	
(A) NAME/KEY: Coding Sequence(B) LOCATION: 6299(D) OTHER INFORMATION:	
(A) NAME/KEY: Modified Base	
(B) LOCATION: 4343 (D) OTHER INFORMATION: Xaa is Ala	
(A) NAME/KEY: Modified Base (B) LOCATION: 8080	

(D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTG Leu	GCC Ala	CTG Leu	CAG Gln	GGG Gly 20	GCT Ala	GCC Ala	AGC Ser	AGA Arg	GCC Ala 25	CAC His	CAG Gln	CAC His	TCC Ser	ATG Met 30	GAG Glu	98
ATC Ile	CGC Arg	ACC Thr	CCC Pro 35	GAC Asp	ATC Ile	AAC Asn	CCT Pro	GCC Ala 40	TGG Trp	TAC Tyr	GCR Xaa	GGC Gly	CGT Arg 45	GGG Gly	ATC Ile	146
							CGG Arg 55									194
CCC Pro	AGG Arg 65	CCT Pro	GGC Gly	CCC Pro	CGG Arg	CGT Arg 70	GTG Val	CCG Pro	GCC Ala	TGC Cys	TTC Phe 75	CGC Arg	CTG Leu	GAA Glu	GGC Gly	242
GGY Xaa 80	GCT Ala	GAG Glu	CCC Pro	TCC Ser	CGA Arg 85	GCC Ala	CTC Leu	CCG Pro	GGG Gly	CGG Arg 90	CTG Leu	ACG Thr	GCC Ala	CAG Gln	CTG Leu 95	290
	CAG Gln		TAAC	AGCG	IGG A	GCCI	GCCC	c cc	ACCC	CTCC	TCC	TCCA	CCA	GCCA	CCTTC	348
ССТС	CAGT	CC I	'AATA	AAAG	C AG	CTGG	CTTG	TT								380

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
 - (A) NAME/KEY: Modified Base
 - (B) LOCATION: 43...43
 - (D) OTHER INFORMATION: Xaa is Ala
 - (A) NAME/KEY: Modified Base
 - (B) LOCATION: 80...80
 - (D) OTHER INFORMATION: Xaa is Gly

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

 Met
 Lys
 Ala
 Val
 Gly
 Ala
 Trp
 Leu
 Leu
 Cys
 Leu
 Leu
 Leu
 Leu
 Gly
 Leu
 Gly
 Leu
 Leu
 Leu
 Leu
 Leu
 Leu
 Gly
 Leu
 L

Arg 65	g Pro	Gly	y Pro	Ar	g Arg	y Va	l Pro	o Ala	а Су	5 Phe	e Arg	J Lei	ı Glı	ı Gl	y Xaa 80	
Ala	Glu	ı Pro	Ser	Arg 85	g Ala	a Lei	ı Pro	Gl _y	/ Arg		ı Thi	Ala	a Gli		u Val	
Glr	ı Glı	ı		03					90					95		
		(2	?) IN	IFORI	(ATIC	ON FO	OR SE	EQ II	NO:	116	:					
	(ERIST se pa									
			TYP					iirs								
							singl	.e								
		(D)	TOP	OLOC	•1: 1	.inea	ır									
	(ix)	FEAT	URE:												
		(A) NA	ME/F	ŒY:	Codi	ng S	eque	nce							
) LO) OT				299 'ION:									
		(۲) NIX	ME / V	EV.	Modi	fied	D	_							
		(B) LO	CATI	ON:	43	.43									
		(D) OT	HER	INFO	RMAT	: NOI	Xaa	is	Ala						
							fied	Bas	е							
) LO) OT:				.80	Xaa	is	Glv						
	1.															
							TION									
GTG	M	TG A et L 1	AG G ys A	CG G la V	al G	GG G ly A 5	CC To	GG C rp L	TC C eu L	TC T eu C 1	ys L	TG C eu L	TG C eu L	TG C eu L	TG GGC eu Gly 15	50
CTG	GCC	CTG	CAG	GGG	GCT	GCC	AGC	AGA	GCC	CAC	CAG	CAC	TCC	ATG	GAG	98
Leu	Ala	Leu	Gln	Gly 20	Ala	Ala	Ser	Arg	Ala 25	His	Gln	His	Ser	Met	Glu	
	~~~								_					30		
Ile	Arg	ACC Thr	Pro	GAC Asp	ATC Ile	AAC Asn	CCT Pro	GCC Ala	TGG	TAC	GCR	GGC	CGT	GGG	ATC	146
			35	•				40		-1-	nuu	Cly	45	GIY	116	
CGG	CCC	GTG	GGC	CGC	TTC	GGC	CGG	CGA	AGA	GCT	GCC	CTG	GGG	GAC	GGA	194
Arg	Pro	Val 50	Gly	Arg	Phe	Gly	Arg	Arg	Arg	Ala	Ala	Leu	Gly	Asp	Gly	
							55					60				
CCC Pro	AGG Ara	CCT	GGC Glv	CCC	CGG	CGT	GTG Val	CCG	GCC	TGC	TTC	CGC	CTG	GAA	GGC	242
	65				5	70	• • • •	110	AIU	Cys	75	Arg	пец	GIU	GIA	
GGY	GCT	GAG	CCC	TCC	CGA	GCC	CTC	CCG	GGG	CGG	CTG	ACG	GCC	CAG	ርፕር	290
Xaa 80	Ala	Glu	Pro	Ser	Arg	Ala	Leu	Pro	Gly	Arg	Leu	Thr	Ala	Gln	Leu	270
J J					85					90					95	

GTC CAG GAA TAACAGCGGG AGCCTGCCCC CCACCCCTCC TCCTCCACCA GCCACCTTC 348

Val Gln Glu

#### (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (ix) FEATURE:
  - (A) NAME/KEY: Modified Base
  - (B) LOCATION: 43...43
  - (D) OTHER INFORMATION: Xaa is Ala
  - (A) NAME/KEY: Modified Base
  - (B) LOCATION: 80...80
  - (D) OTHER INFORMATION: Xaa is Gly

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

 Met
 Lys
 Ala
 Val
 Gly
 Ala
 Trp
 Leu
 Leu
 Cys
 Leu
 Gly
 Leu
 Ala
 Ala
 Ala
 Arg
 Ala
 His
 Gln
 His
 Ser
 Met
 Glu
 Ile
 Ala
 Ile
 Arg
 Ala
 Trp
 Tyr
 Xaa
 Gly
 Arg
 Gly
 Ile
 Arg
 Arg</th

#### (2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 769 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

					CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC	120
					TCCTTGCTAA	180
			TCCCCAGACC			240
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG	300
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG	360

CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA	420
CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	480
AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	540
GCGCTCTTCT	CTCTCTTTCC	AGCCCCGAC	ATCAACCCTG	CCTGGTACGC	600
ATCCGGCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG	660
GGCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC	720
CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA		769
	CGGGTGAACC AGCTGAGCAC GCGCTCTTCT ATCCGGCCCG GGCCCCCGGC	CGGGTGAACC TCCTGTGCGG AGCTGAGCAC ACACCCGGCC GCGCTCTTCT CTCTCTTTCC ATCCGGCCCG TGGGCCGCTT GGCCCCCGGC GTGTGCCGGC	CGGGTGAACC TCCTGTGCGG GTGGGTGGTC AGCTGAGCAC ACACCCGGCC CGGCCACCAG GCGCTCTTCT CTCTCTTTCC AGCCCCCGAC ATCCGGCCCG TGGGCCGCTT CGGCCGGCGA GGCCCCCGGC GTGTGCCGGC CTGCTTCCGC	CGGGTGAACC TCCTGTGCGG GTGGGTGGTC CTGGCATGGC AGCTGAGCAC ACACCCGGCC CGGCCACCAG GGCTGTATGC GCGCTCTTCT CTCTCTTTCC AGCCCCCGAC ATCAACCCTG ATCCGGCCCG TGGGCCGCTT CGGCCGGCGA AGAGCTGCCC	CCTGGTGTGA GTCTGAAATC CTACTTCCCA AAGCCACCCC AGCACCAGAA CGGGTGAACC TCCTGTGCGG GTGGGTGGTC CTGGCATGGC CTGGGCGACA AGCTGAGCA ACACCCGGCC CGGCCACCAG GGCTGTATGC TCCAGGGCAC ATCCGGCCCG TGGGCCGCT CGGCCGGCGA AGAGCTGCCC TGGGGGACGG GGCCCCCGGC GTGTGCCGGC CTGCTTCCGC CTGGAAGGCG GTGCTGAGCC CTCCCGGGGG GGCTGACGC CCAGCTGGTC CAGGAATAA

#### (2) INFORMATION FOR SEQ ID NO:119:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC	120
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	180
GCATCCTGGG	${\tt GTTGGGGTTT}$	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCGGA	240
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG	300
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG	360
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA	420
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA	480
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	540
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCGAC	ATCAACCCTG	CCTGGTACGC	600
AGGCCGTGGG	ATCCGGCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG	660
ACCCAGGCCT	GGCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC	720
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA		769

### (2) INFORMATION FOR SEQ ID NO:120:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG	60
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	CCCCGACAT	CAACCCTGCC	120
TGGTACGCGG	GCCGTGGGAT	CCGGCCCGTG	GGCCGCTTCG	GCCGGCGAAG	AGCTGCCCCG	180
GGGGACGGAC	CCAGGCCTGG	CCCCCGGCGT	GTGCCGGCCT	GCTTCCGCCT	GGAAGGCGGC	240
GCTGAGCCCT	CCCGAGCCCT	CCCGGGGCGG	CTGACGGCCC	AGCTGGTCCA	GGAATAA	297

#### (2) INFORMATION FOR SEQ ID NO:121:

### (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 base pairs

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear															
	(:	ix) 1	FEAT	URE:												
	<ul><li>(A) NAME/KEY: Coding Sequence</li><li>(B) LOCATION: 1294</li><li>(D) OTHER INFORMATION:</li><li>(xi) SEQUENCE DESCRIPTION: SEO ID NO:121:</li></ul>															
		•	_						_							
					GCC Ala											48
					GCC Ala											96
					AAC Asn											144
					GGC Gly											192
					CGT Arg 70											240
					GCC Ala											288
CAG Gln	GAA Glu	TAA														297
		(2)	INE	ORMA	ATION	I FOF	R SEÇ	) ID	NO:1	22:						
	<b>i</b> )	(A) (B) (C)	LENG TYPE STRA	ETH: E: an ANDEI	CHARA 98 a nino ONESS	mino acid : si	aci l .ngle	.ds								
					TYPE											
	(x	xi) S	EQUE	ENCE	DESC	RIPT	: NOI	SEQ	ID	NO:1	.22:					
Met	Lys	Ala	Val	Gly	Ala	Trp	Leu	Leu	Cys	Leu	Leu	Leu	Leu	Gly	Leu	

Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile

20

(B) TYPE: nucleic acid

Arg	Thr	Pro 35	Asp	шe	Asn	Pro	A1a 40	Trp	Tyr	Ala	GIY	Arg	GIY	Ile	Arg	
Pro	Val 50		Arg	Phe	Gly	Arg 55		Arg	Ala	Ala	Leu 60		Asp	Gly	Pro	
Arg 65	Pro	Gly	Pro	Arg	Arg 70	Val	Pro	Ala	Cys	Phe 75	Arg	Leu	Glu	Gly	Gly 80	
		Pro	Ser	Arg 85	Ala	Leu	Pro	Gly	Arg 90	Leu	Thr	Ala	Gln	Leu 95	Val	
Gln	Glu															
		(2)	) INI	FORM	OITA	v FOI	R SE	Q ID	NO:	123:						
	(:	i) SI	EOUE	NCE (	CHAR	ACTEI	RIST	ICS:								
	•	(A)	LENG	GTH:	364 ucle:	base	e pa:									
		(C)	STRA	ANDEI	ONES	S: s:	ingle	e								
					Y: 1:	ıneai	r									
	(:		FEATU													
					EY: (		_	equei	nce							
		(D)	OTI	HER I	INFO	RMAT	ON:									
	(2	ki) S	SEQUI	ENCE	DESC	CRIPT	CION	: SE(	Q ID	NO:	123:					
GGC	ATCA:	rcc <i>i</i>	AGGA <i>l</i>	AGACO	G AC	Мє				s Th					GC TTG /s Leu 10	53
											AGC Ser					101
			Glu					Asp			CCT Pro		Trp			149
			30					35					40			
											AGG Arg					197
		45					50					55				
											TGC Cys					245
	60				1	65	1	02	200	501	70	204		cu		
					TCT Ser				TAAC	ACCC	CCA G	CTCG	AGAA	AG AC	CAGTGC	299
75	_		-		80		3	4								
TGCT		CCC A	AGCC	CACA	C TC	CCTC	TCCC	СТС	CAGA	CCC	TCCT	'CTAC	CC I	CCCI	CTCCT	359 364

	(A) LENGTH: 83 amino acids (B) TYPE: amino acid											
(C) STRANDEDNESS: single (D) TOPOLOGY: linear												
<ul><li>(ii) MOLECULE TYPE: protein</li><li>(v) FRAGMENT TYPE: internal</li></ul>												
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:												
Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Leu Ser Leu Val 1 5 10 15												
Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg 20 25 30												
Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro 35 40 45												
Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly 50 55 60												
Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser 65 70 75 80												
Gln Arg Gly												
(2) INFORMATION FOR SEQ ID NO:125:												
(i) SEQUENCE CHARACTERISTICS:												
<ul><li>(A) LENGTH: 297 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>												
(C) STRANDEDNESS: single												
<del>-</del>												
(D) TOPOLOGY: linear												
(D) TOPOLOGY: linear  (ix) FEATURE:												
(D) TOPOLOGY: linear												
<ul><li>(D) TOPOLOGY: linear</li><li>(ix) FEATURE:</li><li>(A) NAME/KEY: Coding Sequence</li><li>(B) LOCATION: 1297</li></ul>												
(D) TOPOLOGY: linear  (ix) FEATURE:  (A) NAME/KEY: Coding Sequence (B) LOCATION: 1297 (D) OTHER INFORMATION:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  gtg ggc atg gtg ggc aac gtc ctg ctg gtg ctg gtg atc gcg cgg gtg	48											
<ul> <li>(D) TOPOLOGY: linear</li> <li>(ix) FEATURE:</li> <li>(A) NAME/KEY: Coding Sequence</li> <li>(B) LOCATION: 1297</li> <li>(D) OTHER INFORMATION:</li> <li>(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:</li> </ul>	48											
(ix) FEATURE:  (A) NAME/KEY: Coding Sequence (B) LOCATION: 1297 (D) OTHER INFORMATION:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  gtg ggc atg gtg ggc aac gtc ctg ctg gtg atc gcg cgg gtg Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val 1 5 10 15  cgc cgg ctg cac aac gtg acg aac ttc ctc atc ggc aac ctg gcc ttg	<b>48</b> 96											
(ix) FEATURE:  (A) NAME/KEY: Coding Sequence (B) LOCATION: 1297 (D) OTHER INFORMATION:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  gtg ggc atg gtg ggc aac gtc ctg ctg gtg atc gcg cgg gtg Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val 1 5 10 15												
(ix) FEATURE:  (A) NAME/KEY: Coding Sequence (B) LOCATION: 1297 (D) OTHER INFORMATION:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  gtg ggc atg gtg ggc aac gtc ctg ctg gtg ctg gtg atc gcg cgg gtg Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val 1 5 10 15  cgc cgg ctg cac aac gtg acg aac ttc ctc atc ggc aac ctg gcc ttg Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu 20 25 30  tcc gac gtg ctc atg tgc acc gcc tgc gtg ccg ctc acg ctg gcc tat												
(ix) FEATURE:  (A) NAME/KEY: Coding Sequence (B) LOCATION: 1297 (D) OTHER INFORMATION:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  gtg ggc atg gtg ggc aac gtc ctg ctg gtg ctg gtg atc gcg cgg gtg Val Gly Met Val Gly Asn Val Leu Val Leu Val Ile Ala Arg Val 1 5 10 15  cgc cgg ctg cac aac gtg acg aac ttc ctc atc ggc aac ctg gcc ttg Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu 20 25 30	96											
(ix) FEATURE:  (A) NAME/KEY: Coding Sequence (B) LOCATION: 1297 (D) OTHER INFORMATION:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:  gtg ggc atg gtg ggc aac gtc ctg ctg gtg atc gcg cgg gtg Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val 1 5 10 15  cgc cgg ctg cac aac gtg acg aac ttc ctc atc ggc aac ctg gcc ttg Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu 20 25 30  tcc gac gtg ctc atg tgc acc gcc tgc gtg ccg ctc acg ctg gcc tat Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr	96											

gtc ttc ttc ctg cag ccg gtc acc gtc tat gtg tcg gtg ttc acg ctc 240

(i) SEQUENCE CHARACTERISTICS:

Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu 65 70 75 80

acc acc atc gca gtg gac cgg tac gtc gtg ctg gtg cac ccg ctg agg

Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg

85

90

95

cgg cgc atc
Arg Arg Ile

- (2) INFORMATION FOR SEO ID NO:126:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

 Val
 Gly
 Asn
 Val
 Leu
 Leu
 Val
 Leu
 Val
 Ile
 Ala
 Arg
 Val

 1
 5
 Image: Second of the content of the

- (2) INFORMATION FOR SEQ ID NO:127:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 204 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:

Arg Arg Ile

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...204
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ggc ctg ctg ctg gtc acc tac ctg ctc cct ctg ctg gtc atc ctc ctg Gly Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu

48

tct Ser	tac Tyr	gtc Val	cgg Arg 20	gtg Val	tca Ser	gtg Val	aag Lys	ctc Leu 25	cgc Arg	aac Asn	cgc Arg	gtg Val	gtg Val 30	ccg Pro	ggc Gly	9	6
tgc Cys	gtg Val	acc Thr 35	cag Gln	agc Ser	cag Gln	gcc Ala	gac Asp 40	tgg Trp	gac Asp	cgc Arg	gct Ala	cgg Arg 45	cgc Arg	cgg Arg	cgc Arg	144	4
acc Thr	ttc Phe 50	tgc Cys	ttg Leu	ctg Leu	gtg Val	gtg Val 55	gtc Val	gtg Val	gtg Val	gtg Val	ttt Phe 60	gcc Ala	atc Ile	tgc Cys	tgg Trp	192	2
	cct Pro															204	1

15

## (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: amino acid

1

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

### (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 168 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
  (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr 40 Ala Phe Glu Pro Arg Gly Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr Val Tyr Val Ser Val Phe Thr Leu 75 Thr Thr Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg 90 Arg Arg Ile Gly Leu Leu Leu Val Thr Tyr Tyr Leu Leu Pro Leu Leu 105 Val Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg 120 Val Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala 135 140 Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr 165

### (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 228 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr Phe Val Tyr 40 Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys Lys Leu Asn 55 Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe Ser Leu Val 75 Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro Arg Gly Trp 90 Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val Ile Trp Val 105 Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln Ile Leu Thr 115 120 Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys Asp Lys Tyr 135 Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu Ser Tyr Thr 150

#### (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

 Met
 Lys
 Ala
 Val
 Gly
 Ala
 Trp
 Leu
 Leu
 Cys
 Leu
 Leu
 Leu
 Leu
 Leu
 Gly
 Leu
 Gly
 Leu
 Gly
 Leu
 Jis
 Leu
 Leu
 Leu
 Leu
 Gly
 Leu
 Gly
 Leu
 Leu
 Jis
 Jis
 Leu
 Jis
 Jis</th

### (2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

gtggaatgaa ggc	ggtgggg gcctggctcd	tctgcctgct	gctgctgggc	ctggccctgc	60
agggggctgc cag	cagagee caceageact	ccatggagat	ccgcaccccc	gacatcaacc	120
ctgcctggta cgc	gggccgt gggatccggd	ccgtgggccg	cttcggccgg	cgaagagctg	180
ccccggggga cgg	acccagg cctggcccc	ggcgtgtgcc	ggcctgcttc	cgcctggaag	240
gcggcgctga gcc	ctcccga gccctcccgg	ggcggctgac	ggcccagctg	gtccaggaat	300
aacagcggga gcc	tgccccc cacccctcct	cctccaccag	ccaccttccc	tccagtccta	360
ataaaagcag ctg	gcttgtt				380

## (2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 364 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ggcatcatcc	aggaagacgg	agcatggccc	tgaagacgtg	gcttctgtgc	ttgctgctgc	60
		gcttcaagcc				120
cccctgatat	caatcctgcc	tggtacacgg	gccgcgggat	caggcctgtg	ggccgcttcg	180
		agggatgtca				240
tggatggacg	caccaagttc	tctcagcgtg	gataacaccc	cagctcgaga	agacagtgct	300
gctgagccca	agcccacact	ccctgtcccc	tgcagaccct	cctctaccct	ccctctcctc	360
tgct						364

### (2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 361 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

#### (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 24..284
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

ggcctcctcg	ggcctcctcg gaggagccaa ggg atg aag gtg ctg agg gcc tgg ctc ctg tgc Met Lys Val Leu Arg Ala Trp Leu Leu Cys 1 5 10													
ctg ctg at Leu Leu Me	g ctg ggc ctg t Leu Gly Leu 15	gcc ctg cgg Ala Leu Arg	gga gct gca Gly Ala Ala 20	agt cgt acc Ser Arg Thr 25	cat 101 His									
cgg cac to Arg His Se	e atg gag atc Met Glu Ile 30	cgc acc cct Arg Thr Pro 35	Asp Ile Asn	cct gcc tgg Pro Ala Trp 40	tac 149 Tyr									
gcc agt cgc Ala Ser Arc 49	ggg atc agg Gly Ile Arg	cct gtg ggc Pro Val Gly 50	cgc ttc ggt Arg Phe Gly	cgg agg agg Arg Arg Arg 55	gca 197 Ala									
acc ctg ggg Thr Leu Gly	g gac gtc ccc / Asp Val Pro	aag cct ggc Lys Pro Gly 65	ctg cga ccc Leu Arg Pro 70	cgg ctg acc Arg Leu Thr	tgc 245 Cys									

Phe 75		Lev	ı Glu	Gly	Gly 80	' Ala	. Met	Sei	s Se	r Glr 85	n Āsj	p Gl	y Y	acag	ccag	294
	gtca		aact	cact	ct g	gago	ctco	ee ee	cacco	ccaco	c ct	ctcc	tctc	ctt	egggete	354 361
	(2) INFORMATION FOR SEQ ID NO:135:															
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 87 amino acids</li><li>(B) TYPE: amino acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>																
<ul><li>(ii) MOLECULE TYPE: protein</li><li>(v) FRAGMENT TYPE: internal</li></ul>															-	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:																
Met 1	Lys	Val	Leu	Arg 5	Ala	Trp	Leu	Leu	Cys	Leu	Lev	ı Met	Leu	Gly	' Leu	
Ala	Leu	Arg	Gly 20	Ala	Ala	Ser	Arg	Thr 25		Arg	His	Ser	Met		ılle	
Arg	Thr	Pro 35	Asp	Ile	Asn	Pro	Ala 40	Trp	Туг	Ala	Ser	Arg	Gly	Ile	e Arg	
	50					55					60				Pro	
65					70			Thr	Cys	Phe	Pro	Leu	Glu	Gly	Gly 80	
Ala	Met	Ser	Ser	Gln 85	Asp	Gly										
		12	) TN	EODM:	ስጥ <b>ፐ</b> (ጎ	N EO	ח מדי	0 TD	110	726						
	1		) IN: EQUE						NO:	136:						
		(A)	LEN TYP	GTH:	98	amino	o ac									
		(C)	STR	ANDE	ONES	S: s:	ingl	e								
	(		MOLE					in								
			RAGMI			_										
	(2	ki) :	SEQUI	ENCE	DES	CRIP	rion	: SE	Q ID	NO:	136:					
Met 1	Lys	Ala	Val	Gly 5	Ala	Trp	Leu	Leu	Cys 10	Leu	Leu	Leu	Leu	Gly 15	Leu	
Ala	Leu	Gln	Gly 20	Ala	Ala	Ser	Arg	Ala 25		Gln	His	Ser	Met 30		Ile	
Arg	Thr	Pro 35	Asp	Ile	Asn	Pro	Ala 40		Tyr	Ala	Gly	Arg		Ile	Arg	
Pro	Val 50	Gly	Arg	Phe	Gly	Arg 55	Arg	Arg	Ala	Ala	Pro 60		Asp	Gly	Pro	
Arg	Pro	Gly	Pro	Arg	Arg	Val	Pro	Ala	Cys	Arg	Phe	Leu	Glu	Gly	Gly	

65 70 75 80

Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
85 90 95

Gln Glu

### (2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

 Met
 Ala
 Leu
 Lys
 Thr
 Trp
 Leu
 Leu
 Cys
 Leu
 Ser
 Leu
 Val

 Leu
 Pro
 Gly
 Ala
 Ser
 Arg
 Ala
 His
 Gly
 Arg
 Het
 Glu
 Thr
 Arg

 Thr
 Pro
 Asp
 Ile
 Asn
 Pro
 Ala
 Trp
 Trr
 Thr
 Gly
 Arg
 Ala
 Thr
 Pro
 Arg
 Asp
 Val
 Thr
 Gly
 Arg
 Arg
 Pro

 Val
 Gly
 Arg
 Arg
 Arg
 Arg
 Ala
 Thr
 Pro
 Arg
 Asp
 Val
 Thr
 Gly

 Val
 Gly
 Arg
 Arg
 Arg
 Ala
 Thr
 Pro
 Arg
 A

#### (2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

 Met
 Lys
 Val
 Leu
 Arg
 Ala
 Trp
 Leu
 Cys
 Leu
 Leu
 Met
 Leu
 Gly
 Leu

 Ala
 Leu
 Arg
 Thr
 His
 Arg
 His
 Ser
 Met
 Glu
 Ile

 Ala
 Leu
 Arg
 Thr
 His
 Arg
 His
 Ser
 Met
 Glu
 Ile

 Arg
 Thr
 Pro
 Asp
 Ile
 Asn
 Pro
 Ala
 Trp
 Tyr
 Ala
 Ser
 Arg
 Gly
 Ile
 Arg

 Pro
 Val
 Gly
 Arg
 Arg
 Arg
 Arg
 Arg
 Ala
 Thr
 Leu
 Gly
 Asp
 Val
 Pro

 So
 Fro
 Fro
 Arg
 Leu
 Thr
 Leu
 Fro
 Leu
 Gly
 <

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1110
- (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

atg Met 1	acc Thr	tca Ser	ctg Leu	ccc Pro 5	cct Pro	gga Gly	acc Thr	act Thr	999 Gly	Asp	ccc Pro	gat Asp	ttg Leu	ttt Phe	tct Ser	48
gly ggg	ccg Pro	tcg Ser	cca Pro 20	Ala	ggc Gly	tcc Ser	act Thr	cca Pro 25	Ala	aac Asn	cag Gln	g agt Ser	gca Ala 30	Glu	gct Ala	96
tca Ser	gag Glu	agc Ser 35	Asn	gtg Val	tct Ser	gcg Ala	acg Thr 40	Val	ccc	aga Arg	gct Ala	gca Ala 45	gca Ala	gtc Val	acg Thr	144
ccg Pro	ttc Phe 50	cag Gln	agc Ser	ctg Leu	caa Gln	cta Leu 55	gtg Val	cac His	cag Gln	ctg Leu	aag Lys 60	gca Ala	ctg Leu	atc Ile	gtg Val	192
atg Met 65	ctg Leu	tac Tyr	agc Ser	atc Ile	gtg Val 70	gtg Val	gtc Val	gtg Val	ggt Gly	ctg Leu 75	gtg Val	ggc Gly	aac Asn	tgc Cys	ctt Leu 80	240
ctt Leu	gtg Val	ctg Leu	gtg Val	atc Ile 85	gcg Ala	cgc Arg	gtg Val	cgc Arg	cgg Arg 90	ctg Leu	cac His	aac Asn	gtg Val	acc Thr 95	aac Asn	288
ttc Phe	ctc Leu	atc Ile	ggc Gly 100	aac Asn	ctg Leu	gcc Ala	ttg Leu	tcc Ser 105	gat Asp	gtg Val	ctc Leu	atg Met	tgt Cys 110	gcc Ala	gcc Ala	336
tgt Cys	gtg Val	cct Pro 115	ctc Leu	acg Thr	ctg Leu	gcc Ala	tac Tyr 120	gcc Ala	ttt Phe	gaa Glu	cct Pro	cgt Arg 125	ggc Gly	tgg Trp	gtg Val	384
ttc Phe	ggt Gly 130	gga Gly	ggc Gly	ctg Leu	tgc Cys	cac His 135	ctt Leu	gtt Val	ttc Phe	ttc Phe	ctg Leu 140	cag Gln	ccg Pro	gtc Val	acc Thr	432
gtc Val 145	tac Tyr	gta Val	tcg Ser	gtg Val	ttc Phe 150	aca Thr	ctc Leu	acc Thr	aca Thr	atc Ile 155	gct Ala	gtg Val	gac Asp	cgc Arg	tat Tyr 160	480

												ctg Leu				528
gcc Ala	tac Tyr	gct Ala	gtg Val 180	ctg Leu	ggc Gly	atc Ile	tgg Trp	gct Ala 185	cta Leu	tct Ser	gca Ala	gtg Val	ctg Leu 190	gcg Ala	ctg Leu	576
												ccc Pro 205				624
												cag Gln				672
												ccc Pro				720
												cgg Arg				768
gtg Val	cct Pro	ggc Gly	agc Ser 260	gtg Val	acc Thr	cag Gln	agc Ser	cag Gln 265	gct Ala	gac Asp	tgg Trp	gac Asp	cga Arg 270	gcg Ala	cgt Arg	816
cgc Arg	cgt Arg	cgc Arg 275	act Thr	ttc Phe	tgc Cys	ctg Leu	ctg Leu 280	gtg Val	gtg Val	gtg Val	gtg Val	gtc Val 285	gtg Val	ttc Phe	gcg Ala	864
												cgg Arg				912
												cag Gln				960
cac His	tgg Trp	ctt Leu	gcc Ala	atg Met 325	agc Ser	tcc Ser	gcc Ala	tgc Cys	tac Tyr 330	aac Asn	ccc Pro	ttc Phe	atc Ile	tat Tyr 335	gcg Ala	1008
												atg Met				1056
tgg Trp	ccc Pro	cgc Arg 355	aag Lys	atc Ile	gtg Val	cct Pro	cat His 360	ggc Gly	cag Gln	aat Asn	atg Met	acc Thr 365	gtc Val	agt Ser	gtg Val	1104
gtc Val	atc Ile 370	tgat	ga													1116

## (2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 370 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

1				5					10					15	Ser
Gly	Pro	Ser	Pro 20	Ala	Gly	Ser	Thr	Pro 25	Ala	Asn	Gln	Ser	Ala 30	Glu	Ala
		35					40					45		Val	
	50					55					60			Ile	
65					70					75				Cys	80
				85					90					Thr 95	
			100					105					110	Ala	
		115					120					125	_	Trp	
	130					135					140			Val	
145					150					155				Arg	160
				165					170					Leu 175	
			180					185					190	Ala	
		195					200					205		Asp	
	210					215					220		_	Gln	
225					230					235				Leu	240
				245					250					Arg 255	
			260					265					270	Ala	
		275					280					285		Phe	
	290					295					300			Leu	_
305					310					315				Leu	320
His	Trp	Leu	Ala	Met 325	Ser	Ser	Ala	Cys	Tyr 330	Asn	Pro	Phe	Ile	Tyr 335	Ala